

Note that the generation of T cells and/or antibodies can also be accomplished by administering cells, preferably treated to be rendered non-proliferative, which present relevant T cell or B cell epitopes for response, such as the epitopes discussed supra.

The therapeutic approaches may also include antisense therapies, wherein an antisense molecule, preferably from 10 to 100 nucleotides in length, is administered to the subject either "neat" or in a carrier, such as a liposome, to facilitate incorporation into a cell, followed by inhibition of expression of the protein. Such antisense sequences may also be incorporated into appropriate vaccines, such as in viral vectors (e.g., Vaccinia), bacterial constructs, such as variants of the known BCG vaccine, and so forth.

Other features and applications of the invention will be clear to the skilled artisan, and need not be set forth herein. The terms and expression which have been employed are used as terms of description and not of limitation, and there is no intention in the use of such terms and expression of excluding any equivalents of the features shown and described or portions thereof, it being recognized that various modifications are possible within the scope of the invention.

We claim:

1. Isolated nucleic acid molecule which encodes a cancer associated antigen, whose amino acid sequence is identical to the amino acid sequence encoded by the nucleotide sequence of SEQ ID NO: 1, 3, 4, 8, 15, 19, 22, or 26.
2. The isolated nucleic acid molecule of claim 1, comprising the nucleotide sequence of SEQ ID NO: 1.
3. The isolated nucleic acid molecule of claim 1, comprising the nucleotide sequence of SEQ ID NO: 3.
4. The isolated nucleic acid molecule of claim 1, comprising the nucleotide sequence of SEQ ID NO: 4.
5. The isolated nucleic acid molecule of claim 1, comprising the nucleotide sequence of SEQ ID NO: 8.
6. The isolated nucleic acid molecule of claim 1, comprising the nucleotide sequence of SEQ ID NO: 15.
7. The isolated nucleic acid molecule of claim 1, comprising the nucleotide sequence of SEQ ID NO: 19.
8. The isolated nucleic acid molecule of claim 1, comprising the nucleotide sequence of SEQ ID NO: 22.
9. The isolated nucleic acid molecule of claim 1, comprising the nucleotide sequence of SEQ ID NO: 26.
10. Expression vector comprising the isolated nucleic acid molecule of claim 1, operably linked to a promoter.

11. Eukaryotic cell line or prokaryotic cell strain, transformed or transfected with the expression vector of claim 10.
12. Isolated cancer associated antigen comprising all or part of the amino acid sequence encoded by SEQ ID NO: 1, 3, 4, 8, 15, 19, 22 or 26.
13. Eukaryotic cell line or prokaryotic cell strain, transformed or transfected with the isolated nucleic acid molecule of claim 1.
14. The eukaryotic cell line or prokaryotic cell strain of claim 13, wherein said cell line is also transfected with a nucleic acid molecule coding for a cytokine.
15. The eukaryotic cell line or prokaryotic cell strain of claim 14, wherein said cell line is further transfected by a nucleic acid molecule coding for an MHC molecule.
16. The eukaryotic cell line or prokaryotic cell strain of claim 14, wherein said cytokine is an interleukin.
17. The eukaryotic cell line or prokaryotic cell strain of claim 16, wherein said interleukin is IL-2, IL-4 or IL-12.
18. The eukaryotic cell line or prokaryotic cell strain of claim 13, wherein said cell line has been rendered non-proliferative.
19. The eukaryotic cell line of claim 13, wherein said cell line is a fibroblast cell line.
20. Expression vector comprising a mutated or attenuated virus and the isolated nucleic acid molecule of claim 1.
21. The expression vector of claim 20, wherein said virus is adenovirus or vaccinia virus.
22. The expression vector of claim 21, wherein said virus is vaccinia virus.
23. The expression vector of claim 21, wherein said virus is adenovirus.

24. Expression system useful in transfecting a cell, comprising (i) a first vector containing a nucleic acid molecule which codes for the isolated cancer associated antigen of claim 13 and (ii) a second vector selected from the group consisting of (a) a vector containing a nucleic acid molecule which codes for an MHC or HLA molecule which presents an antigen derived from said cancer associated antigen and (b) a vector containing a nucleic acid molecule which codes for an interleukin.

25. Immunogenic composition comprising the isolated cancer antigen of claim 12, and a pharmaceutically acceptable adjuvant.

26. The immunogenic composition of claim 25, wherein said adjuvant is a cytokine, a saponin, or GM-CSF.

27. Immunogenic composition comprising at least one peptide consisting of an amino acid sequence of from 8 to 12 amino acids concatenated to each other in the isolated cancer associated cancer antigen of claim 12, and a pharmaceutically acceptable adjuvant.

28. The immunogenic composition of claim 27, wherein said adjuvant is a saponin, a cytokine, or GM-CSF.

29. The immunogenic composition of claim 25, wherein said composition comprises a plurality of peptides which complex with a specific MHC molecule.

30. Immunogenic composition which comprises at least one expression vector which encodes a peptide derived from the amino acid sequence encoded by SEQ ID NO: 1, 3, 4, 8, 15, 19, 22 or 26.

31. The immunogenic composition of claim 30, wherein said at least one expression vector codes for a plurality of peptides.

32. Vaccine useful in treating a subject afflicted with a cancerous condition comprising the isolated eukaryotic cell line of claim 13 and a pharmacologically acceptable adjuvant.

33. The vaccine of claim 32, wherein said eukaryotic cell line has been rendered non-proliferative.

34. The vaccine of claim 33, wherein said eukaryotic cell line is a human cell line.

35. A composition of matter useful in treating a cancerous condition comprising a non-proliferative cell line having expressed on its surface a peptide derived from the amino acid sequence encoded by SEQ ID NO: 1, 3, 4, 8, 15, 19, 22 or 26.

36. The composition of matter of claim 35, wherein said cell line is a human cell line.

37. A composition of matter useful in treating a cancerous condition, comprising (i) a peptide derived from the amino acid sequence encoded by SEQ ID NO: 1, 3, 4, 8, 15, 19, 22 or 26, (ii) an MHC or HLA molecule, and (iii) a pharmaceutically acceptable carrier.

38. Isolated antibody which is specific for the cancer associated antigen of claim 12.

39. The isolated antibody of claim 38, wherein said antibody is a monoclonal antibody.

40. Method for screening for cancer in a sample, comprising contacting said sample with a nucleic acid molecule which hybridizes to all or part of the molecule encoded by SEQ ID NO: 1, 2, 3, 4, 8, 15, 19, 22 or 26 and determining hybridization as an indication of cancer cells in said sample.

41. A method for screening for cancer in a sample, comprising contacting said sample with the isolated antibody of claim 38, and determining binding of said antibody to a target as an indicator of cancer.

42. Method for diagnosing a cancerous condition in a subject, comprising contacting an immune reactive cell containing sample of said subject to a cell line transfected with the isolated nucleic acid molecule of claim 1, and determining interaction of said transfected cell line with said immunoreactive cell, said interaction being indicative of said cancer condition.

43. A method for determining regression, progression or onset of a cancerous condition comprising monitoring a sample from a patient with said cancerous condition for a parameter selected from the group consisting of (i) a protein encoded by SEQ ID NO: 1, 2, 3, 4, 8, 15, 19, 22 or 26, (ii) a peptide derived from said protein, (iii) cytolytic T cells specific for said peptide and an MHC molecule with which it non-covalently complexes, and (iv) antibodies specific for said CT protein, wherein amount of said parameter is indicative of progression or regression or onset of said cancerous condition.

44. The method of claim 43, wherein said sample is a body fluid or exudate.

45. The method of claim 43, wherein said sample is a tissue.

46. The method of claim 43, comprising contacting said sample with an antibody which specifically binds with said protein or peptide.

47. The method of claim 46, wherein said antibody is labelled with a radioactive label or an enzyme.

48. The method of claim 46, wherein said antibody is a monoclonal antibody.

49. The method of claim 43, comprising amplifying RNA which codes for said protein.

50. The method of claim 49, wherein said amplifying comprises carrying out polymerase chain reaction.

51. The method of claim 42, comprising contacting said sample with a nucleic acid molecule which specifically hybridizes to a nucleic acid molecule which codes for or expresses said protein.

52. The method of claim 49, wherein said nucleic acid molecule comprises SEQ ID NO: 9, 10, 11, 12, 13, 14, 17, 18, 20, 21, 24, 25, 28 or 29.

53. The method of claim 43, comprising assaying said sample for shed protein.

54. The method of claim 43, comprising assaying said sample for antibodies specific for said protein, by contacting said sample with protein.

55. Method for diagnosing a cancerous condition comprising assaying a sample taken from a subject for an immunoreactive cell specific for a peptide derived from a protein encoded by SEQ ID NO: 1, 2, 3, 4, 8, 15, 19, 22 or 26, complexed to an MHC molecule, presence of said immunoreactive cell being indicative of said cancerous condition.

56. Composition comprising at least one peptide consisting of an amino acid sequence of from 8 to 25 amino acids concatenated to each other in the isolated cancer associated antigen of claim 12, and a pharmaceutically acceptable adjuvant.

57. The composition of claim 56, wherein said adjuvant is a saponin, a cytokine, or GM-CSF.

58. The composition of claim 56, comprising a plurality of MHC binding peptides.

59. Composition comprising an expression vector which encodes at least one peptide consisting of an amino acid sequence of from 8 to 25 amino acids concatenated to each other in the isolated cancer associated antigen of claim 12, and pharmaceutically acceptable adjuvant.

60. The composition of claim 59, wherein said expression vector encodes a plurality of peptides.

61. A method for screening for possible presence of a pathological condition, comprising assaying a sample from a patient believed to have a pathological condition for antibodies specific to at least one of the cancer associated antigens encoded by SEQ ID NOS: 1, 2, 3, 4, 8, 15, 19, 22 or 26, presence of said antibodies being indicative of possible presence of said pathological condition.

62. The method of claim 61, wherein said pathological condition is cancer.

63. The method of claim 61, wherein said cancer is melanoma.

64. The method of claim 61, further comprising contacting said sample to purified cancer associated antigen encoded by SEQ ID NO: 1, 3, 4, 8, 15, 19, 22 or 26.

65. A method for screening for possible presence of a pathological condition in a subject, comprising assaying a sample taken from said subject for expression of a nucleic acid molecule, the nucleotide sequence of which comprises SEQ ID NO: 1, 2, 3, 4, 8, 15, 19, 22 or 26, expression of said nucleic acid molecule being indicative of possible presence of said pathological condition.

66. The method of claim 65, wherein said pathological condition is cancer.

67. The method of claim 65, comprising determining expression via polymerase chain reaction.

68. The method of claim 65, comprising determining expression by contacting said sample with at least one of SEQ ID NO: 9, 10, 11, 12, 13, 14, 17, 18, 20, 21, 24, 25, 28 or 29.

69. A method for determining regression, progression of onset of a cancerous condition comprising monitoring a sample from a patient with said cancerous condition for a parameter selected from the group consisting of (i) a cancer associated antigen encoded by SEQ ID NO: 1, 2, 3, 4, 8, 15, 19, 22 or 25, (ii) a peptide derived from said cancer associated antigen,

(iii) cytolytic T cells specific for said peptide and an MHC molecule with which it non-covalently complexes, and (iv) antibodies specific for said cancer associated antigen, wherein amount of said parameter is indicative of progression or regression or onset of said cancerous condition.

70. The method of claim 69, wherein said sample is a body fluid or exudate.
71. The method of claim 69, wherein said sample is a tissue.
72. The method of claim 69, comprising contacting said sample with an antibody which specifically binds with said protein or peptide.
73. The method of claim 72, wherein said antibody is labelled with a radioactive label or an enzyme.
74. The method of claim 72, wherein said antibody is a monoclonal antibody.
75. The method of claim 69, comprising amplifying RNA which codes for said protein.
76. The method of claim 75, wherein said amplifying comprises carrying out polymerase chain reaction.
77. The method of claim 69, comprising contacting said sample with a nucleic acid molecule which specifically hybridizes to a nucleic acid molecule which codes for or expresses said protein.
78. The method of claim 69, comprising assaying said sample for shed cancer associated antigen.
79. The method of claim 69, comprising assaying said sample for antibodies specific for said cancer associated antigen, by contacting said sample with said cancer associated antigen.

80. Method for screening for a cancerous condition comprising assaying a sample taken from a subject for an immunoreactive cell specific for a peptide derived from a cancer associated antigen encoded by SEQ ID NO: 1, 2, 3, 4, 8, 15, 19, 22 or 26, complexed to an MHC molecule, presence of said immunoreactive cell being indicative of said cancerous condition.

81. An isolated nucleic acid molecule consisting of a nucleotide sequence defined by SEQ ID NO: 1, 2, 3, 8, 15, 19, 22 or 26.

82. Isolated nucleic acid molecule the complimentary sequence of which hybridizes, under stringent conditions, to the nucleotide sequence set forth in SEQ ID NO: 4, 5, 8, 15, 19, 22 or 26.

83. An isolated polypeptide comprising at least 9 consecutive amino acids set forth in SEQ ID NO: 5, 7, 16, 19, 23, 27, or 30.

84. The isolated polypeptide of claim 83, comprising at least 9 consecutive amino acids set forth in SEQ ID NO: 23 or 30.

85. The isolated polypeptide of claim 84, comprising at least 9 consecutive amino acids of the amino acid sequence set forth in SEQ ID NO: 23.

86. The isolated polypeptide of claim 85, comprising amino acids 102-111, 904-912 or 1262-1270 of SEQ ID NO: 23.

87. An isolated nucleic acid molecule which encodes the amino acid sequence of SEQ ID NO: 30.

88. An isolated nucleic acid molecule which encodes the isolated polypeptide of claim 86.

89. Expression vector comprising the isolated nucleic acid molecule of claim 88, operably linked to a promoter.

<110> Jager, Dirk
Scanlan, Matthew
Gure, Ali
Jager, Elke
Knuth, Alexander
Old, Lloyd
Chen, Yao-tseng

<120> Isolated Nucleic Acid Molecules Encoding Cancer Associated Antigens, the Antigens per se, and Uses Thereof

<130> IUD 5615.2PCT

<140>

<141>

<150> US 09/451,739

<151> 2000-06-22

<150> US 09/451,739

<151> 1999-11-30

<160> 30

<210> 1
<211> 1533
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> 236
<400> 1
ggttttccac gttggacaag tggggcttgg cggccagcgg agcgcggccca ttcccgctgc 60
ccgcgtcgat cctcttttcc accccggccca gtggggcgat gggcggcgccg ggcggcgccgg 120
ctggggccctc tcccgccgggt gtgtgcgcgc tcgtacgcgc ggcccccggc gccaggccccg 180
ccgcctgaga gggggccctgc gcegcggggcc ggggggtgcg cccgggagcc acggncacccg 240
cgccccccgcg cctcaggccgc tggggtcccccc gggggccggc agggcgccggc cggggctccggc 300
agatgttagcc gcccggccca agcaggaggcc ggggggggggg cccggggaga gcgaggggctt 360
tgcattttgc agtgctatit tttggggggg ggggggggtg gggggatgc gaaaggccgg 420
cccgatgcgc ggggaccccc ggggtgaacc atgttgatgc ctgcacacccg ggaggcagatc 480
caacctggta actatgtggc ggactacccgt gactccatcg agtccctggc tttagacttg 540
cagagaaaatg ttcgtcgat gccccggatgc gacgcgaaat accaaaggat cctgaaggag 600
ctagacgagt gtcacggccg cttcagtcgc gagacagacy gggcgccagaa gggccggatg 660
ctgcactgtg tgcaggccgc gtcgtatccgc agccaggaggc tggggcgcgcgaa gaagatcccg 720
atcggtggcc agatgggtggc gtcgtggggag aaccgcacccg ggcagggtggc cagccacgtg 780
gagctttcg aggcgcagcc ggaggctggc gacacaggcc gcaacaggccg caaggctggc 840
ggggacaggcc ccaaaaggccg ggcggccaggc caggctgaca agcccaacccg caaggccgtca 900
ccggccggccgc gcaacaaacccg gaaacgtggc gacgcgtccca gcaaccacccg ccacccggac 960
ggcgccctccg gcacacccaa ggagaagaag gccaagaccc ccaagaagaa gaaggcgatcc 1020
aaaggccaaagg cggaggcgaga ggcgtccctc gccgaccccc ccatcgaccc caacggaccc 1080

acgtactgtc tggcaaccca ggtctccat ggggagatga tcggctgcga caacgacgag 1140
 tgccccatcg agtgggttcca cttctctgtc gtggggctca atcataaaacc caaggccaag 1200
 tggtactgtc ccaagtgcgg gggggagaac gagaagacca tggacaaagc cctggagaaa 1260
 tccaaaaaaag agagggctta caacaggttag tttgtggaca ggccctgtgt gtggggagga 1320
 ccaaataaac cgtgtattta ttacattgtc gcttttgtg aggtgcagg agtgtaaaaat 1380
 gtatattttt aaagaatgtt agaaaaaggaa ccattccctt catagggatc gcagtgtttc 1440
 tggtttgcctt ttgttttcat tggtacacgt gtascaagaa agtggctgtt ggatcagcat 1500
 ttttagaaaact acaaataatag gtttgattca aca 1533

<210> 2
 <211> 1143
 <212> DNA
 <213> Homo sapiens
 <400> 2
 gagtaaccccg ataatatgcc gttgtccggc acggcgacga gaatccccag atatagcagt 60
 agcagtgtatc cccggccctgt ggctcgggggc cgggggtgtca gtccggacccg cctcccgccg 120
 cccggggggg ctccggagaca gtttcaggcc gcatactttgc tgaccggagg gtggggccgc 180
 gctgtggccgt ggaaacacat cctgaaggag cttagacgatg gctacggcggc ctccgtcg 240
 gagacacagc gggcgccagaa gggggggatc ctgcactgtg tgcagccggc gctgtccgc 300
 agccaggaga cttggcgacga aaagatccag atcgtgaccc agatggtggc gctgggtggag 360
 aaccgcacgc ggcagggtggc cagccacgtg gagttgttcg agggcgccgc ggggtggc 420
 gacacagtgg gcaacacggc caagggttggc gctggacccggc ccaatggcgc tgcggtagcc 480
 cagtctgaca agcccaacacg caagccgttca cggccggcggc gcaacaacgc gaaccgttgc 540
 aacgcgttca gcaaccacgc ccacgacgc gggccctgg gcacacccaa ggagaagaaag 600
 gccaagaccc ccaagaagaa gaagccgttcc aaggccaaagg cggagccgaga gggttccct 660
 gcccacccctt cccatcgaccc caacgaccc acgtactgtc tggcaaccca ggttccctat 720
 ggggagatga tggctgcga caacgacgag tggccatcg agtgggttcca cttctctgtc 780
 gtggggctca atcataaaacc caagggcaag tggtaactgtc ccaagtgcgg gggggagaaac 840
 gagaagacca tggacaaagc cctggagaaa tccaaaaaaag agagggctta caacaggttag 900
 tttgtggaca ggcggctgtgt gtggggagga caaaataaac cgtgtatttt ttacattgtc 960
 gcttttgttgc aggtgcagg agtgcataat gtatattttt aaagaatgtt agaaaaggaa 1020
 ccattccctt catagggatc gcagtgtttc tggtttcat tggtacacgt 1080
 gtaacaagaa agtggctgtgt ggatcagcat ttttagaaaact acaaataatag gtttgattca 1140
 aca 1143

<210> 3
 <211> 742
 <212> DNA
 <213> Homo sapiens
 <400> 3
 cgcgcgttccac accccagccg cccgtacgtc gtcccccctgg cggccctggc ctctggaaaa 60
 agtgacccaggc aaggccacgc cccggccaggc gccggccctgg agcccgccgc ccccgaggcc 120

tgggacgaga tcctgaagga gctagacgag tgcacgagc gcttcagtcg cgagacagac 180
 ggggcgcaga agccggcgat gctgcactgt gtgcagcgcg cgctgatccg cagccaggag 240
 ctgggcgacg agaagatcca gatcgtgagc cagatggtgg agctgggtga gaacogcacg 300
 cggcaggtgg acagccacgt ggagctgttc gagggcgcgc aggagctggg cgacacagcg 360
 ggcacacagcg gcaaggctgg cgcggacagg cccaaaggcg aggccggcgcg gcaggctgac 420
 aagccccaca gcaagcgttc acggccggcag cgcaacaaacg agaaccgtga gaacgcgttc 480
 agcaaccacg accacgacga cggccgcctcg ggcacaccca aggagaagaa ggccaaagacc 540
 tccaaagaaga agaagcgttc caaggccaaag gcccggcgag aggctccctc tgccgacotc 600
 cccatcgacc ccaaccaacc cacgctactgt ctgtcaacc aggtctccctt tggggagatg 660
 atcggctgcg acaacgacga gtgcggccatc gagtggttcc acttctcggt cgtggggctc 720
 aatcataaac ccaagggcaa gt 742

<210> 4
 <211> 857
 <212> DNA
 <213> Homo sapiens
 <400> 4
 cctccggagaa cggtgtccat ggcacagggc gggaaagagat aaggcctagg gaaggccccc 60
 ctccggccctt tccacccctt ctggggctcg gcacttagaa gcagcttccc tccaggcccc 120
 ctttgtctcc aaggcggttcc aaacttagta cccggagacg acacaaaggg agggccgggtga 180
 cggatggcgc aggcggggga gcccgttggg ctgtctgggg tgggtggcccg gcccgggaaat 240
 ggagatcttg aaggagctag acgagtgctt cggagcgatc agtcgcgaga cagacggggc 300
 gcaagaagggg cggatgtgtc actgtgtgca ggcggcgctg atcccgccccc aggagctggg 360
 cgacgagaag atccagatcg tgagccatg ggtggagctg gtggagaacc gcaacgccc 420
 ggtggacagc cacgtggagc tggccggggc gcaaggccggc ctggccggccca cagcggggca 480
 cagcggccaa gctggccggg acaggcccaa aggccggcg gcaacggccagg ctgacaagccc 540
 caacagcaag cgcgtccacggc ggcaggccaa caacgagaac cgtggccggcc cgtccggccaa 600
 ccacgacac gacggccggc cctggccaccc accaaaggag aagaaggccaa agacccctccaa 660
 gaagaagaag cgcgtccaaagg ccaaggccggc gcaaggccggc tccctggcccg acctcccccatt 720
 cgaccccaac gaccccccgt actgtgtgtc caaccggcc tccatgggg agatgtatgg 780
 ctgcgacaaac gacgagtgcc ccatcgagtg gttccacttc tctgtccgtgg ggcccaatca 840
 taaacccaaag ggcaagt 857

<210> 5
 <211> 279
 <212> PRT
 <213> Homo sapiens
 <400> 5
 Met Leu Ser Pro Ala Asn Gly Glu Gln Leu His Leu Val Asn Tyr Val
 1 5 10 15

Gln Asp Tyr Leu Asp Ser Ile Glu Ser Leu Pro Phe Asp Leu Gln Arg
 20 25 30

Asn Val Ser Leu Met Arg Glu Ile Asp Ala Lys Tyr Gln Glu Ile Leu
 35 40 45

Lys Glu Leu Asp Glu Cys Tyr Glu Arg Phe Ser Arg Glu Thr Asp Gly
 50 55 60
 Ala Gln Lys Arg Arg Met Leu His Cys Val Gln Arg Ala Leu Ile Arg
 65 70 75 80
 Ser Gln Glu Leu Gly Asp Glu Lys Ile Gln Ile Val Ser Gln Met Val
 85 90 95
 Glu Leu Val Glu Asn Arg Thr Arg Gln Val Asp Ser His Val Glu Leu
 100 105 110
 Phe Glu Ala Gln Gln Glu Leu Gly Asp Thr Val Gly Asn Ser Gly Lys
 115 120 125
 Val Gly Ala Asp Arg Pro Asn Gly Asp Ala Val Ala Gln Ser Asp Lys
 130 135 140
 Pro Asn Ser Lys Arg Ser Arg Arg Gln Arg Asn Asn Glu Asn Arg Glu
 145 150 155 160
 Asn Ala Ser Ser Asn His Asp His Asp Gly Ala Ser Gly Thr Pro
 165 170 175
 Lys Glu Lys Lys Ala Lys Thr Ser Lys Lys Lys Lys Arg Ser Lys Ala
 180 185 190
 Lys Ala Glu Arg Glu Ala Ser Pro Ala Asp Leu Pro Ile Asp Pro Asn
 195 200 205
 Glu Pro Thr Tyr Cys Leu Cys Asn Gln Val Ser Tyr Gly Glu Met Ile
 210 215 220
 Gly Cys Asp Asn Asp Glu Cys Pro Ile Glu Trp Phe His Phe Ser Cys
 225 230 235 240
 Val Gly Leu Asn His Lys Pro Lys Gly Lys Trp Tyr Cys Pro Lys Cys
 245 250 255
 Arg Gly Glu Asn Glu Lys Thr Met Asp Lys Ala Leu Glu Lys Ser Lys
 260 265 270
 Lys Glu Arg Ala Tyr Asn Arg
 275

<210> 5
 <211> 210
 <212> PRT
 <213> Homo sapiens
 <400> 5
 Met Leu His Cys Val Gln Arg Ala Leu Ile Arg Ser Gln Glu Leu Gly
 1 5 10 15
 Asp Glu Lys Ile Gln Ile Val Ser Gln Met Val Glu Leu Val Glu Asn
 20 25 30
 Arg Thr Arg Gln Val Asp Ser His Val Glu Leu Phe Glu Ala Gln Gln
 35 40 45
 Glu Leu Gly Asp Thr Val Gly Asn Ser Gly Lys Val Gly Ala Asp Arg
 50 55 60
 Pro Asn Gly Asp Ala Val Ala Gln Ser Asp Lys Pro Asn Ser Lys Arg
 65 70 75 80
 Ser Arg Arg Gln Arg Asn Asn Glu Asn Arg Glu Asn Ala Ser Ser Asn
 85 90 95
 His Asp His Asp Asp Gly Ala Ser Gly Thr Pro Lys Glu Lys Lys Ala
 100 105 110

Lys Thr Ser Lys Lys Lys Lys Arg Ser Lys Ala Lys Ala Glu Arg Glu
 115 120 125
 Ala Ser Pro Ala Asp Leu Pro Ile Asp Pro Asn Glu Pro Thr Tyr Cys
 130 135 140
 Ieu Cys Asn Gln Val Ser Tyr Gly Glu Met Ile Gly Cys Asp Asn Asp
 145 150 155 160
 Glu Cys Pro Ile Glu Trp Phe His Phe Ser Cys Val Gly Leu Asn His
 165 170 175
 Lys Pro Iys Gly Lys Trp Tyr Cys Pro Lys Cys Arg Gly Glu Asn Glu
 180 185 190
 Lys Thr Met Asp Lys Ala Leu Glu Lys Ser Lys Lys Glu Arg Ala Tyr
 195 200 205
 Asn Arg
 210

<210> 7
 <211> 235
 <212> PRT
 <213> Homo sapiens
 <400> 7
 Met Glu Ile Leu Lys Glu Leu Asp Glu Cys Tyr Glu Arg Phe Ser Arg
 1 5 10 15
 Glu Thr Asp Gly Ala Gln Lys Arg Arg Met Leu His Cys Val Gln Arg
 20 25 30
 Ala Leu Ile Arg Ser Gln Glu Leu Gly Asp Glu Lys Ile Gln Ile Val
 35 40 45
 Ser Gln Met Val Glu Leu Val Glu Asn Arg Thr Arg Gln Val Asp Ser
 50 55 60
 His Val Glu Leu Phe Glu Ala Gln Gln Glu Leu Gly Asp Thr Val Gly
 65 70 75 80
 Asn Ser Gly Lys Val Gly Ala Asp Arg Pro Asn Gly Asp Ala Val Ala
 85 90 95
 Gln Ser Asp Lys Pro Asn Ser Lys Arg Ser Arg Arg Gln Arg Asn Asn
 100 105 110
 Glu Asn Arg Glu Asn Ala Ser Ser Asn His Asp His Asp Asp Gly Ala
 115 120 125
 Ser Gly Thr Pro Lys Glu Lys Lys Ala Lys Thr Ser Lys Lys Lys
 130 135 140
 Arg Ser Lys Ala Lys Ala Glu Arg Glu Ala Ser Pro Ala Asp Leu Pro
 145 150 155 160
 Ile Asp Pro Asn Glu Pro Thr Tyr Cys Leu Cys Asn Gln Val Ser Tyr
 165 170 175
 Gly Glu Met Ile Gly Cys Asp Asn Asp Gln Cys Pro Ile Glu Trp Phe
 180 185 190
 His Phe Ser Cys Val Gly Leu Asn His Lys Pro Lys Gly Lys Trp Tyr
 195 200 205
 Cys Pro Lys Cys Arg Gly Glu Asn Glu Lys Thr Met Asp Lys Ala Leu
 210 215 220
 Glu Lys Ser Lys Lys Glu Arg Ala Tyr Asn Arg
 225 230 235

<210> 8
 <211> 772
 <212> DNA
 <213> Homo sapiens
 <221> CDS
 <222> 695,714
 <400> 8
 aaagcgttct cggcgccggc gcaacaacta gaaccgttag aacgcgttcca gcaaccggcg 60
 cccacgacga cgtcacctcg ggcacgccccca aggagaagaa agcccaagacc tcttaagaaga 120
 agcaggcgctc catggccaaay gcgtagccggc agggcgccccc cgcagacccctc cccatcgacc 180
 ccagcgagcc ctctctactgg .yagatgtatcc gatcgccatca cgaatgcggcc atcgactgtgt 240
 tcccgctctc gtgtgttagt ctcaaccata aaccaaaagcg caagtggtagc tgttccagat 300
 gcccgggaaa gaacgatggg caaagccctt gageagtccca gaaaaaaaac agggcttata 360
 acaggtagtt tggggacatgt cgtataatag tgaggagaac aaaataaagcc agtgtgttga 420
 ttacattgtcc acctttgtcg aggtgcaggaa agtgtaaaat gtatattttt aaagaatgtt 480
 gtttagaggcc gggcgccgtg gctcaagccct gtaatcccg cactttggga ggcggaggcg 540
 gtcggatcac gaggtcaggaa gatcgagacc atccctggctt acacggtgaa accccgtctc 600
 tactaaaaat tcaaaaaaaaaa aattagctgg gctgtggcc gggcgccgtt agtcccaagct 660
 attcgggagg ctgaggcagg agaatggcc gAACCTGGGA ggtggagctt gcaatgagcc 720
 aaggtagcgc cactgcactc cagccctggcc gacagagoga gactccatct ta 772

<210> 9
 <211> 32
 <212> DNA
 <213> Homo sapiens
 <400> 9
 cacacaggat ccatgtgttag tccctgcggaaat gg 32

<210> 10
 <211> 23
 <212> DNA
 <213> Homo sapiens
 <400> 10
 cgtggtcgtg gtgtgtggac gcg 23

<210> 11
 <211> 21
 <212> DNA
 <213> Homo sapiens
 <400> 11
 cccagcgcccttctgacgtgtt c 21

<210> 12
 <211> 23
 <212> DNA
 <213> Homo sapiens
 <400> 12
 cgtggtcgtg gttgtgtggac gcg 23

<210> 13
 <211> 23
 <212> DNA
 <213> Homo sapiens
 <400> 13

ggaaaggagata agggcccttgggg aag 23

aaatccanaa gcttaasat taatctcaat tatgcaggag atgtcttaag agaasataca 1680
 ttggtttcag gaacatgcac aaagagacca acgtgaaaca cagtgtcaa tgaaggaage 1740
 tgaacacatg tntcaaaancg aacaagatna tgtgaaceaa cacactganc agcaggagtc 1800
 tctagatcaag aaatttatttc aactacaag caaaaatatg tggttcaac agcaattagt 1860
 tcatgcacat aangaaagct gacaacaaa gcaagataac aattgtatattt catntcttg 1920
 agaggaataat gcnatcata ttctaaaga gaaasatgeg gagatattt attachataa 1980
 ccatttaaaa aacccgtata tttcaatatg gaaaaaaa anaaaaaaa 2030

<210> 16

<211> 513

<212> PRT

<213> Homo sapiens

<400> 16

Met	Lys	Val	Ser	Ile	Pro	Thr	Lys	Ala	Ile	Glu	Leu	Met	Asp	Met	Gln
1															

Thr	Phe	Lys	Ala	Glu	Pro	Pro	Glu	Lys	Pro	Ser	Ala	Phe	Glu	Pro	Ala

Ile	Glu	Met	Gln	Lys	Ser	Val	Pro	Asn	Lys	Ala	Leu	Glu	Leu	Lys	Asn
35															

Glu	Gln	Thr	Ile	Arg	Ala	Asp	Glu	Ile	Leu	Pro	Ser	Glu	Ser	Lys	Gln
50															

Lys	Asp	Tyr	Glu	Glu	Glu	Ser	Ser	Trp	Asp	Ser	Glu	Ser	Leu	Cys	Glu	Thr
65																

Val	Ser	Gln	Lys	Asp	Val	Cys	Leu	Pro	Lys	Ala	Thr	His	Gln	Lys	Glu
85															

Ile	Asp	Lys	Ile	Asn	Gly	Ile	Glu	Gln	Ser	Pro	Asp	Asn	Asp	Gly
100														

Phe	Leu	Lys	Ala	Pro	Cys	Arg	Met	Lys	Val	Ser	Ile	Pro	Thr	Lys	Ala
115															

Leu	Glu	Leu	Met	Asp	Met	Gln	Thr	Phe	Lys	Ala	Glu	Pro	Pro	Glu	Lys
130															

Pro	Ser	Ala	Phe	Glu	Pro	Ala	Ile	Glu	Met	Gln	Lys	Ser	Val	Pro	Asn
145															

Lys	Ala	Ile	Glu	Leu	Lys	Asn	Glu	Gln	Thr	Leu	Arg	Ala	Asp	Gln	Met
165															

Phe	Pro	Ser	Glu	Ser	Lys	Gln	Lys	Val	Glu	Gln	Asn	Ser	Trp	Asp
180														

Ser	Glu	Ser	Leu	Arg	Glu	Thr	Val	Ser	Gln	Lys	Asp	Val	Cys	Val	Pro
195															

Lys	Ala	Thr	His	Gln	Lys	Glu	Met	Asp	Lys	Ile	Ser	Gly	Ile	Glu
210														

Asp	Ser	Thr	Ser	Leu	Ser	Ile	Glu	Asp	Thr	Val	His	Ser	Cys	Glu
225														

Arg	Ala	Arg	Glu	Leu	Gln	Lys	Asp	His	Cys	Glu	Gln	Arg	Thr	Gly	Lys
245															

Met	Glu	Gln	Met	Lys	Lys	Phe	Cys	Val	Leu	Lys	Lys	Leu	Ser
260													

Glu	Ala	Lys	Gln	Ile	Lys	Ser	Gln	Leu	Glu	Asn	Gln	Lys	Val	Lys	Trp

275	280	285
Glu Gln Glu Leu Cys Ser Val Arg Leu Thr Leu Asn Gln Gln Glu Glu		
290	295	300
Lys Arg Arg Asn Ala Asp Ile Leu Asn Glu Lys Ile Arg Gln Glu Leu		
305	310	315
Gly Arg Ile Glu Glu Gln His Arg Lys Glu Leu Glu Val Lys Gln Gln		
325	330	335
Leu Glu Gln Ala Leu Arg Ile Gln Asp Ile Glu Leu Lys Ser Val Glu		
340	345	350
Ser Asn Leu Asn Gln Val Ser His Thr His Glu Asn Glu Asn Tyr Leu		
355	360	365
Leu His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu		
370	375	380
Glu Ile Ala Thr Leu Lys His Gln Tyr Gln Glu Lys Glu Asn Lys Tyr		
385	390	395
Phe Glu Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala Glu Leu Gln Met		
405	410	415
Thr Leu Lys Leu Lys Glu Gln Ser Leu Thr Lys Arg Ala Ser Gln Tyr		
420	425	430
Ser Gly Gln Leu Lys Val Leu Ile Ala Glu Asn Thr Met Leu Thr Ser		
435	440	445
Lys Leu Lys Glu Lys Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile Glu		
450	455	460
Ser His His Pro Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile		
465	470	475
Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp		
485	490	495
Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser Ser Thr Asp Ile		
500	505	510

.

<210> 17
<211> 33
<212> DNA
<213> Homo sapiens
<400> 17
cacacaggat ccatgcaggc cccgcacaaag gag 33

<210> 18
<211> 34
<212> DNA
<213> Homo sapiens
<400> 18
cacacaaagc ttcttagatt tggcacagcc agag 34

<210> 19
<211> 294
<212> PRT
<213> Homo sapiens
<400> 19
Met Pro Leu Cys Thr Ala Thr Arg Ile Pro Arg Tyr Ser Ser Ser Ser
1 S 10 15

Asp Pro Gly Pro Val Ala Arg Gly Arg Gly Cys Ser Ser Asp Arg Leu
20 25 30

Pro Arg Pro Ala Gly Pro Ala Arg Arg Gln Phe Gln Ala Ala Ser Ieu
 35 40 45
 Ieu Thr Arg Gly Trp Gly Arg Ala Trp Pro Trp Lys Gln Ile Ieu Lys
 50 55 60
 Glu Leu Asp Glu Cys Tyr Glu Arg Phe Ser Arg Glu Thr Asp Gly Ala
 65 70 75 80
 Gln Lys Arg Arg Met Leu His Cys Val Gln Arg Ala Leu Ile Arg Ser
 85 90 95
 Gln Glu Leu Gly Asp Glu Lys Ile Gln Ile Val Ser Gln Met Val Glu
 100 105 110
 Leu Val Glu Asn Arg Thr Arg Gln Val Asp Ser His Val Glu Leu Phe
 115 120 125
 Glu Ala Gln Gln Glu Leu Gly Asp Thr Val Gly Asn Ser Gly Lys Val
 130 135 140
 Gly Ala Asp Arg Pro Asn Gly Asp Ala Val Ala Gln Ser Asp Lys Pro
 145 150 155 160
 Asn Ser Lys Arg Ser Arg Arg Gln Arg Asn Asn Glu Asn Arg Glu Asn
 165 170 175
 Ala Ser Ser Asn His Asp His Asp Asp Gly Ala Ser Gly Thr Pro Lys
 180 185 190
 Glu Lys Lys Ala Lys Thr Ser Lys Lys Lys Lys Arg Ser Lys Ala Lys
 195 200 205
 Ala Glu Arg Glu Ala Ser Pro Ala Asp Leu Pro Ile Asp Pro Asn Glu
 210 215 220
 Pro Thr Tyr Cys Leu Cys Asn Gln Val Ser Tyr Gly Glu Met Ile Gly
 225 230 235 240
 Cys Asp Asn Asp Glu Cys Pro Ile Glu Trp Phe His Phe Ser Cys Val
 245 250 255
 Gly Leu Asn His Lys Pro Lys Gly Lys Trp Tyr Cys Pro Lys Cys Arg
 260 265 270
 Gly Glu Asn Glu Lys Thr Met Asp Lys Ala Leu Glu Lys Ser Lys Lys
 275 280 285
 Glu Arg Ala Tyr Asn Arg
 290 294

<210> 20
 <211> 22
 <212> DNA
 <213> Homo sapiens
 <400> 20
 caaaggcagag cctcccgaga 22

<210> 21
 <211> 24
 <212> DNA
 <213> Homo sapiens
 <400> 21
 cctatgtgc ttttcgattc ttcc 24

<210> 22
 <211> 4115
 <212> DNA
 <213> Homo sapiens
 <400> 22

ctagtctata cagcaacgac cttacatcgt cactctgggg tcttagaaag tccataaago 60
 tgcctcccg gacaaggccg aagctggaga gatgacaaag ggaagaagac atcaacatca 120
 atataacaaga gcccagaaga gactgtctca actggccctg gtcaatggcc tgaggaagta 180
 gtaacatcgc ggttagacaga agtgcgcagct gacgtcttg tggcgcacac ggacacactct 240
 gatgaaggct tcaaatgcac caggaggctt tgcaaatatt tgatagatc ggtgcgcata 300
 tcaatctgt gatgtgtatc caacatggct tccattatgc gtttatagtg gatcttgcata 360
 gtggtgccaa actgtgtcc atggcgcagt atcgaagtgc caacaaggct gcctcacaccc 420
 acttttacta ccataacgaa acaagtgcgc aattgtggaa ttttgcgtat aaaaatgcac 480
 atgcgaatgc gitaataagt taaatgcaca cccatgtct gctgtatgc tggatcatca 540
 gagatagttt catgttttgc agcaaaatgt gacgtcttg tgcagatata gtggagtaac 600
 tgcagaacat atgcgttttc tggatgttc tccatcatc aaaaattatc gatataatac 660
 gaaaattatc aaaaatcata aataaccatc cagaaggaac tctgcaggaa acctgtatgc 720
 gctgcacccct ggccggaaaga cacctgcacac gctgaaagct ggtggaaaaa cacctgtatc 780
 ggctgcaccc tggatggaaag acaccgtaca ggctgaaagc tggatggaaaaa acacctgtatc 840
 aggctgcata ttggatggagg aacatctgc aattcaatc ttggagaaaag gacatctgg 900
 aagtttgcac gtcagcggaa aacacccatc gaaattacgc tcctgcacaa aacatgtca 960
 gaaattttacg gtcagcggaa ggaagacata gaagatgcac gggagaaaaa gaagacacac 1020
 ctagggaaat atgagtcccg aaaaagaaaca ctgagaaatt acgtggccag aaaaaggaaaga 1080
 ccttaggaaga cgcgtggag aaaaagaaac cctgtaaaga tggatgcgtg caagatgtac 1140
 atctaatata ctaaagtttt gaaaaaggaa atctaaatgc tttgcgttcc aaaaaagaat 1200
 catctacaaa gcaagtgcac tggatggagg tccatcaga tccasacaag ggaagatgaa 1260
 gaatattttt tgattctcggt gtcttttgc agtttgcac gattcaatgt gtatacctgc 1320
 gtctatataat aaaaagtsat gagatataa agaagtagaa agcctccata aagccatctg 1380
 cttcaagcc gccattggaa gcaaaactct ttccaaataa gcccatttgc gaaatgtaa 1440
 caaacattgc agcagatccg tggatggagg gaaatccacaa aaaggactat aagaaaaatc 1500
 ttggatgttct agatgttgc gagactgtttt acagaaggat tggatgttcc aaggctacac 1560
 ataaaaaaga atagataaaa aatggaaaaa tggatggatc cttatataat tggatgttgc 1620
 aaggctaccc cggaaatgaaa ttctatccactaaaggctt agaattgtaa acatgcacac 1680
 ttccaaagcc agcctccggg aagccatctg ctccgagccctt ccactgaaat caaaagtctg 1740
 tcccaataa gcccatttgc gaaaaatgaa aacatggag gcaatgtata actccatca 1800
 gaaatccaaac aaaggactat aagaaaaatc tggatgttgc gagactgttgc 1860
 acagaaggat tggatgttcc aaggctgccc tcaaaaagaa tagatataat aatggaaaaat 1920
 tggatggatc cttatataat tggatgttgc aggttgcactg ggaatgttcc tttatattcc 1980
 actaaaggctt agaattgtatc acatgcacac ttccaaagcc gcccatttgc agcctccatcc 2040
 ctccgagccctt ccactgaaat caaaagtctg tccasataaa cttggatgttcc aagaatgtac 2100
 aacatgtatc gcaatgtata actccatca aatccaaacaa aaggactatc agaaatgttcc 2160

〈210〉 23

211 1343

<212> PRT

<213> *Homo sapiens*

<400> 23

Met The 3

1	5	10	15
Lys Arg Thr Ala Leu His Trp Ala Cys Val Asn Gly His Glu Glu Val			
20	25	30	
Val Thr Phe Leu Val Asp Arg Lys Cys Gln Leu Asp Val Leu Asp Gly			
35	40	45	
Glu His Arg Thr Pro Leu Met Lys Ala Leu Gln Cys His Gln Glu Ala			
50	55	60	
Cys Ala Asn Ile Leu Ile Asp Ser Gly Ala Asp Ile Asn Leu Val Asp			
65	70	75	80
Val Tyr Gly Asn Met Ala Leu His Tyr Ala Val Tyr Ser Glu Ile Leu			
85	90	95	
Ser Val Val Ala Lys Leu Leu Ser His Gly Ala Val Ile Glu Val His			
100	105	110	
Asn Lys Ala Ser Leu Thr Pro Leu Leu Leu Ser Ile Thr Lys Arg Ser			
115	120	125	
Glu Gln Ile Val Glu Phe Leu Leu Ile Lys Asn Ala Asn Ala Asn Ala			
130	135	140	
Val Asn Lys Tyr Lys Cys Thr Ala Leu Met Leu Ala Val Cys His Gly			
145	150	155	160
Ser Ser Glu Ile Val Gly Met Leu Leu Gln Gln Asn Val Asp Val Phe			
165	170	175	
Ala Ala Asp Ile Cys Gly Val Thr Ala Glu His Tyr Ala Val Thr Cys			
180	185	190	
Gly Phe His His Ile His Glu Gln Ile Met Glu Tyr Ile Arg Lys Leu			
195	200	205	
Ser Lys Asn His Gln Asn Thr Asn Pro Glu Gly Thr Ser Ala Gly Thr			
210	215	220	
Pro Asp Glu Ala Ala Pro Leu Ala Gln Arg Thr Pro Asp Thr Ala Glu			
225	230	235	240
Ser Leu Val Glu Lys Thr Pro Asp Glu Ala Ala Pro Leu Val Glu Arg			
245	250	255	
Thr Pro Asp Thr Ala Glu Ser Leu Val Glu Lys Thr Pro Asp Glu Ala			
260	265	270	
Ala Ser Leu Val Glu Gly Thr Ser Asp Lys Ile Gln Cys Leu Glu Lys			
275	280	285	
Ala Thr Ser Gly Lys Phe Glu Gln Ser Ala Glu Glu Thr Pro Arg Glu			
290	295	300	
Ile Thr Ser Pro Ala Lys Glu Thr Ser Glu Lys Phe Thr Trp Pro Ala			
305	310	315	320
Lys Gly Arg Pro Arg Lys Ile Ala Trp Glu Lys Lys Glu Asp Thr Pro			
325	330	335	
Arg Glu Ile Met Ser Pro Ala Lys Glu Thr Ser Glu Lys Phe Thr Trp			
340	345	350	
Ala Ala Lys Gly Arg Pro Arg Lys Ile Ala Trp Glu Lys Lys Glu Thr			
355	360	365	
Pro Val Lys Thr Gly Cys Val Ala Arg Val Thr Ser Asn Lys Thr Lys			
370	375	380	
Val Leu Glu Lys Gly Arg Ser Lys Met Ile Ala Cys Pro Thr Lys Glu			

385	390	395	400
Ser Ser Thr Lys Ala Ser Ala Asn Asp Gln Arg Phe Pro Ser Glu Ser			
405	410	415	
Lys Gln Glu Glu Asp Glu Glu Tyr Ser Cys Asp Ser Arg Ser Ile Phe			
420	425	430	
Glu Ser Ser Ala Lys Ile Gln Val Cys Ile Pro Glu Ser Ile Tyr Gln			
435	440	445	
Lys Val Met Glu Ile Asn Arg Glu Val Glu Glu Pro Pro Lys Lys Pro			
450	455	460	
Ser Ala Phe Lys Pro Ala Ile Glu Met Gln Asn Ser Val Pro Asn Lys			
465	470	475	480
Ala Phe Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Pro Met Phe			
485	490	495	
Pro Pro Glu Ser Lys Gln Lys Asp Tyr Glu Glu Asn Ser Trp Asp Ser			
500	505	510	
Glu Ser Leu Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys			
515	520	525	
Ala Thr His Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Glu			
530	535	540	
Ser Pro Asn Lys Asp Gly Leu Leu Lys Ala Thr Cys Gly Met Lys Val			
545	550	555	560
Ser Ile Pro Thr Lys Ala Leu Glu Leu Lys Asp Met Gln Thr Phe Lys			
565	570	575	
Ala Glu Pro Pro Gly Lys Pro Ser Ala Phe Glu Pro Ala Thr Glu Met			
580	585	590	
Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr			
595	600	605	
Trp Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr			
610	615	620	
Glu Glu Asn Ser Trp Asp Thr Glu Ser Leu Cys Glu Thr Val Ser Gln			
625	630	635	640
Lys Asp Val Cys Leu Pro Lys Ala Ala His Gln Lys Glu Ile Asp Lys			
645	650	655	
Ile Asn Gly Lys Leu Glu Gly Ser Pro Val Lys Asp Gly Leu Ile Lys			
660	665	670	
Ala Asn Cys Gly Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu Leu			
675	680	685	
Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro Ser Ala			
690	695	700	
Phe Glu Pro Ala Ile Gln Met Gln Lys Ser Val Pro Asn Lys Ala Leu			
705	710	715	720
Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser			
725	730	735	
Glu Ser Lys Gln Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser			
740	745	750	
Leu Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Thr			
755	760	765	
His Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Gln Ser Pro			

770	775	780
Asp Asn Asp Gly Phe Leu Lys Ala Pro Cys Arg Met Lys Val Ser Ile		
785	790	795
Pro Thr Lys Ala Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu		
805	810	815
Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys		
820	825	830
Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg		
835	840	845
Ala Asp Gln Met Phe Pro Ser Glu Ser Lys Gln Lys Lys Val Glu Glu		
850	855	860
Asn Ser Trp Asp Ser Glu Ser Leu Arg Glu Thr Val Ser Gln Lys Asp		
865	870	875
Val Cys Val Pro Lys Ala Thr His Gln Lys Glu Met Asp Lys Ile Ser		
885	890	895
Gly Lys Leu Glu Asp Ser Thr Ser Leu Ser Lys Ile Leu Asp Thr Val		
900	905	910
His Ser Cys Glu Arg Ala Arg Glu Leu Gln Lys Asp His Cys Glu Gln		
915	920	925
Arg Thr Gly Lys Met Glu Gln Met Lys Lys Phe Cys Val Leu Lys		
930	935	940
Lys Lys Leu Ser Glu Ala Lys Glu Ile Lys Ser Gln Leu Glu Asn Gln		
945	950	955
Lys Val Lys Trp Glu Gln Glu Leu Cys Ser Val Arg Leu Thr Leu Asn		
965	970	975
Gln Glu Glu Lys Arg Arg Asn Ala Asp Ile Leu Asn Glu Lys Ile		
980	985	990
Arg Glu Glu Leu Gly Arg Ile Glu Glu Gln His Arg Lys Glu Leu Glu		
995	1000	1005
Val Lys Gln Gln Leu Glu Gln Ala Leu Arg Ile Gln Asp Ile Glu Leu		
1010	1015	1020
Lys Ser Val Glu Ser Asn Leu Asn Gln Val Ser His Thr His Glu Asn		
1025	1030	1035
1040		
Glu Asn Tyr Leu Leu His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala		
1045	1050	1055
Met Leu Lys Leu Glu Ile Ala Thr Leu Lys His Gln Tyr Gln Glu Lys		
1060	1065	1070
Glu Asn Lys Tyr Phe Glu Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala		
1075	1080	1085
Glu Leu Gln Met Thr Leu Lys Leu Lys Glu Glu Ser Leu Thr Lys Arg		
1090	1095	1100
Ala Ser Gln Tyr Ser Gly Gln Leu Lys Val Ile Ala Glu Asn Thr		
1105	1110	1115
1120		
Met Leu Thr Ser Lys Leu Lys Glu Lys Gln Asp Lys Glu Ile Leu Glu		
1125	1130	1135
Ala Glu Ile Glu Ser His His Pro Arg Leu Ala Ser Ala Val Gln Asp		
1140	1145	1150
His Asp Gln Ile Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His		

1155	1160	1165
Ile Ala Gly Asp Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser		
1170	1175	1180
Ser Thr Ile Tyr Asn Asn Glu Val Leu His Gln Pro Leu Ser Glu Ala		
1185	1190	1195
Gln Arg Lys Ser Lys Ser Leu Lys Ile Asn Leu Asn Tyr Ala Gly Asp		
1205	1210	1215
Ala Leu Arg Glu Asn Thr Leu Val Ser Glu His Ala Gln Arg Asp Gln		
1220	1225	1230
Arg Glu Thr Gln Cys Gln Met Lys Glu Ala Gln His Met Tyr Gln Asn		
1235	1240	1245
Glu Gln Asp Asn Val Asn Lys His Thr Glu Gln Gln Glu Ser Leu Asp		
1250	1255	1260
Gln Lys Leu Phe Gln Leu Gln Ser Lys Asn Met Trp Leu Gln Gln Gln		
1265	1270	1275
Leu Val His Ala His Lys Lys Ala Asp Asn Lys Ser Lys Ile Thr Ile		
1280	1285	1290
Asp Ile His Phe Leu Gln Arg Lys Met Gln His His Leu Leu Lys Glu		
1295	1300	1310
Lys Asn Gln Glu Ile Phe Asn Tyr Asn Asn His Leu Lys Asn Arg Ile		
1315	1320	1325
Tyr Gln Tyr Glu Lys Glu Lys Ala Glu Thr Glu Asn Ser		
1330	1335	1340

<210> 24
 <211> 22
 <212> DNA
 <213> Homo sapiens
 <400> 24
 aatgggaaca agagctctgc ag 22

<210> 25
 <211> 23
 <212> DNA
 <213> Homo sapiens
 <400> 25
 gggatcatctg aagttcagca ttc 23

<210> 26
 <211> 3673
 <212> DNA
 <213> Homo sapiens
 <221> CDS
 <222> 439, 473, 1769
 <400> 26
 caagagatgg cgcatacaga aatttctgtt ggtgttgggg cgggtgcggg aactgaagac 60
 gggcggatgtc gagccgggggg cgggtgtctgg ggaagggtaa gcggggaaagcg agggcgagg 120
 gtaggggctg gggaaaggcg agcggggaggc gggggatctc tcttagcaggc ggctgcagcc 180
 atgaagaggc ttttagctgc cgctggcaag ggcgtgcggg gcccggagcc cccgaacccc 240
 ttcaagcgttacac tgagaaggac tacggggacca ttacttccgg ggatcttaggg 300
 aagatccata cagctgcctc cggggccaa gtccagaagc tggagaagat gacagtaggg 360
 aagaagcccg tcaacctgaa caaaagagat atgaagaaga ggactgtct acactggcc 420

tggtagatcc acattcagtc tttttggcaa accgactact gaaaattcac agtctacaaa 2640
 agttgaggaa gacttttaatc ttactaccaa ggagggagca acaaagacag taactggaca 2700
 acaggaacgt gatattggca ttattgaacg agtccacaa gatcaaccaa ataaatgtcc 2760
 cacatcagaa ttaggaagaa aagaagatac aaaaatcaact tcagattctg agattatctc 2820
 tgtgagtgtat acacagaatt atgagtgttt acctgaggtt acatataaaa aagaatataaa 2880
 gacaacaaat ggccaaaatag aagagtctcc tgaaaangct tctcacttig agectyccac 2940
 taaaatgcaa aactctgttc caaaataaagg cttagaatgg aagaatataac aaacatttag 3000
 agcagattca actaccatca caaaaatctt ggatgcactt ccttcttgcg aaagaggaag 3060
 ggaacttaaa aaagataact gtgaacaaat tacagcaaaa atggacaaa tggaaatataa 3120
 gttttgtta ctacaaaagg aactgtcaga agcgaagaa ataaaatcac agttagagaa 3180
 ccaszaagct asatgggaac aagagcttgc csgtgrgaga ttgcctttaa atcaagaaga 3240
 agagaagaga agaaatgtcg statatataaa agaaaaattt agacccgaag agcaacttag 3300
 gaaaatgtta gaagtgaaac accaacttga acagactctc agaatacacaat ataaaaattt 3360
 gaaaatgtta acaagtaatt tgaatcaggt ttctcactt catgaaatgtt aaaaatgtat 3420
 ctttcatgaa aattgcattgt tggaaaagga aattgcattg ctaaaactgg aagtagccac 3480
 actgaaacat caacaccagg tgaaggaaaa taatacttt gaggacatta agatittaca 3540
 agaaaaaaat gctgaaacttc aatgtgaccct aaaaactgaaa cagaacacag taacaaaaag 3600
 ggcatttcag tatagagagc agcttaaagt tctgacggca gagaacacga tgcgtgacttc 3660
 taaattgaaag gaa 3673

<210> 27

<211> 1011

<212> PRT

<213> Homo sapiens

<400> 27

Met	Val	Ala	Thr	Leu	Leu	Ser	Tyr	Gly	Ala	Val	Ile	Glu	Val	Gln	Asn
1															

Lys	Ala	Ser	Leu	Thr	Fro	Leu	Leu	Ala	Ile	Gln	Lys	Arg	Ser	Lys
20														

Gin	Thr	Val	Glu	Phe	Leu	Leu	Thr	Lys	Asn	Ala	Asn	Ala	Asn	Ala	Phe
35															

Asn	Glu	Ser	Lys	Cys	Thr	Ala	Leu	Met	Leu	Ala	Ile	Cys	Glu	Gly	Ser
50															

Ser	Glu	Ile	Val	Gly	Met	Leu	Leu	Gln	Gln	Asn	Val	Asp	Val	Phe	Ala
65															

Glu	Asp	Ile	His	Gly	Ile	Thr	Ala	Glu	Arg	Tyx	Ala	Ala	Ala	Arg	Gly
85															

Val	Asn	Tyr	Ile	His	Gln	Gln	Leu	Leu	Glu	His	Ile	Arg	Lys	Leu	Pro
100															

Lys	Asn	Pro	Gln	Asn	Thr	Asn	Pro	Glu	Gly	Thr	Ser	Thr	Gly	Thr	Pro
115															

Asp	Gln	Ala	Ala	Pro	Leu	Ala	Glu	Arg	Thr	Pro	Asp	Thr	Ala	Glu	Ser
130															

Leu	Leu	Glu	Lys	Thr	Fro	Asp	Glu	Ala	Ala	Arg	Leu	Val	Glu	Gly	Thr

145	150	155	160
Ser Ala Lys Ile Gln Cys Leu Gly Lys Ala Thr Ser Gly Lys Phe Glu			
165	170	175	
Gln Ser Thr Glu Glu Thr Pro Arg Lys Ile Leu Arg Pro Thr Lys Glu			
180	185	190	
Thr Ser Glu Lys Phe Ser Trp Pro Ala Lys Glu Arg Ser Arg Lys Ile			
195	200	205	
Thr Trp Glu Glu Lys Glu Thr Ser Val Lys Thr Glu Cys Val Ala Gly			
210	215	220	
Val Thr Pro Asn Lys Thr Glu Val Leu Glu Lys Gly Thr Ser Asn Met			
225	230	235	240
Ile Ala Cys Pro Thr Lys Glu Thr Ser Thr Lys Ala Ser Thr Asn Val			
245	250	255	
Asp Val Ser Ser Val Gln Pro Ile Phe Ser Leu Phe Gly Thr Arg Thr			
260	265	270	
Ile Glu Asn Ser Gln Cys Thr Lys Val Glu Glu Asp Phe Asn Leu Ala			
275	280	285	
Thr Lys Ile Ile Ser Lys Ser Ala Ala Gln Asn Tyr Thr Cys Leu Pro			
290	295	300	
Asp Ala Thr Tyr Gln Lys Asp Ile Lys Thr Ile Asn His Lys Ile Glu			
305	310	315	320
Asp Gln Met Phe Pro Ser Glu Ser Lys Arg Glu Gln Asp Gln Glu Tyr			
325	330	335	
Ser Trp Asp Ser Gly Ser Leu Phe Glu Ser Ser Ala Lys Thr Gln Val			
340	345	350	
Cys Ile Pro Glu Ser Met Tyr Gln Lys Val Met Glu Ile Asn Arg Glu			
355	360	365	
Val Glu Glu Leu Pro Glu Lys Pro Ser Ala Phe Lys Pro Ala Val Glu			
370	375	380	
Met Gln Lys Thr Val Pro Asn Lys Ala Phe Glu Leu Lys Asn Glu Gln			
385	390	395	400
Thr Leu Arg Ala Ala Gln Met Phe Pro Ser Glu Ser Lys Gln Lys Asp			
405	410	415	
Asp Glu Glu Asn Ser Trp Asp Ser Glu Ser Pro Cys Glu Thr Val Ser			
420	425	430	
Gln Lys Asp Val Tyr Leu Pro Lys Ala Thr His Gln Lys Glu Phe Asp			
435	440	445	
Thr Leu Ser Gly Lys Leu Glu Gln Ser Pro Val Lys Asp Gly Leu Leu			
450	455	460	
Lys Pro Thr Cys Gly Arg Lys Val Ser Leu Pro Asn Lys Ala Leu Glu			
465	470	475	480
Leu Lys Asp Arg Glu Thr Phe Lys Ala Glu Ser Pro Asp Lys Asp Gly			
485	490	495	
Leu Leu Lys Pro Thr Cys Gly Arg Lys Val Ser Leu Pro Asn Lys Ala			
500	505	510	
Leu Glu Leu Lys Asp Arg Glu Thr Leu Lys Ala Glu Ser Pro Asp Asn			
515	520	525	
Asp Gly Leu Leu Lys Pro Thr Cys Gly Arg Lys Val Ser Leu Pro Asn			

530	535	540
Lys Ala Leu Glu Leu Lys Asp Arg Glu Thr Phe Lys Ala Ala Gln Met		
545	550	555
Phe Pro Ser Glu Ser Lys Glu Asp Asp Glu Glu Asn Ser Trp Asp		
560	565	570
575		
Phe Glu Ser Phe Leu Glu Thr Leu Leu Gln Asn Asp Val Cys Leu Pro		
580	585	590
Lys Ala Thr His Gln Lys Glu Phe Asp Thr Leu Ser Gly Lys Leu Glu		
595	600	605
Glu Ser Pro Asp Lys Asp Gly Leu Leu Lys Pro Thr Cys Gly Met Lys		
610	615	620
Ille Ser Leu Pro Asn Lys Ala Leu Glu Leu Lys Asp Arg Glu Thr Phe		
625	630	635
640		
Lys Ala Glu Asp Val Ser Ser Val Glu Ser Thr Phe Ser Leu Phe Gly		
645	650	655
Lys Pro Thr Thr Glu Asn Ser Gln Ser Thr Lys Val Glu Glu Asp Phe		
660	665	670
Asn Leu Thr Thr Lys Glu Gly Ala Thr Lys Thr Val Thr Gly Gln Gln		
675	680	685
Glu Arg Asp Ille Gly Ille Glu Arg Ala Pro Gln Asp Gln Thr Asn		
690	695	700
Lys Met Pro Thr Ser Gln Leu Gly Arg Lys Glu Asp Thr Lys Ser Thr		
705	710	715
720		
Ser Asp Ser Glu Ille Ille Ser Val Ser Asp Thr Gln Asn Tyr Glu Cys		
725	730	735
Leu Pro Glu Ala Thr Tyr Gln Lys Glu Ille Lys Thr Thr Asn Gly Lys		
740	745	750
Ille Glu Glu Ser Pro Glu Lys Pro Ser His Phe Glu Pro Ala Thr Glu		
755	760	765
Met Gln Asn Ser Val Pro Asn Lys Gly Leu Glu Trp Lys Asn Lys Gln		
770	775	780
Thr Leu Arg Ala Asp Ser Thr Thr Leu Ser Lys Ille Leu Asp Ala Leu		
785	790	795
800		
Pro Ser Cys Glu Arg Gly Arg Glu Leu Lys Lys Asp Asn Cys Glu Gln		
805	810	815
Ille Thr Ala Lys Met Glu Gln Met Lys Asn Lys Phe Cys Val Leu Gln		
820	825	830
Lys Glu Leu Ser Glu Ala Lys Glu Ille Lys Ser Gln Leu Glu Asn Gln		
835	840	845
Lys Ala Lys Trp Glu Gln Glu Leu Cys Ser Val Arg Leu Pro Leu Asn		
850	855	860
Gln Glu Glu Glu Lys Arg Arg Asn Val Asp Ille Leu Lys Glu Lys Ille		
865	870	875
880		
Arg Pro Glu Glu Gln Leu Arg Lys Lys Leu Glu Val Lys His Gln Leu		
885	890	895
Glu Gln Thr Leu Arg Ille Gln Asp Ille Glu Leu Lys Ser Val Thr Ser		
900	905	910
Asn Leu Asn Gln Val Ser His Thr His Glu Ser Glu Asn Asp Leu Phe		

915	920	925
His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu Glu		
930	935	940
Val Ala Thr Leu Lys His Gln His Gln Val Lys Glu Asn Lys Tyr Phe		
945	950	955
Glu Asp Ile Lys Ile Leu Gln Glu Lys Asn Ala Glu Leu Gln Met Thr		
965	970	975
Leu Lys Leu Lys Gln Lys Thr Val Thr Lys Arg Ala Ser Gln Tyr Arg		
980	985	990
Glu Gln Leu Lys Val Leu Thr Ala Glu Asn Thr Met Leu Thr Ser Lys		
995	1000	1005
Leu Lys Glu		
1010		

<210> 28
 <211> 23
 <212> DNA
 <213> Homo sapiens
 <400> 28
 ttcatacat gctggtgctg atc 23

<210> 29
 <211> 24
 <212> DNA
 <213> Homo sapiens
 <400> 29
 cccagacatt gaatittggc agac 24

<210> 30
 <211> 56
 <212> PRT
 <213> Homo sapiens
 <400> 30

Met Glu Glu Ile Ser Ala Ala Ala Val Lys Val Val Pro Gly Pro Glu
 1 5 10 15

Arg Pro Ser Pro Phe Ser Gln Leu Val Tyr Thr Ser Asn Asp Ser Tyr
 20 25 30

Ile Val His Ser Gly Asp Leu Arg Lys Ile His Lys Ala Ala Ser Arg
 35 40 45

Gly Gln Val Arg Lys Leu Glu Lys
 50 55